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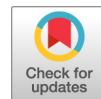
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Complete Genome Sequence of *Shewanella* sp. WE21, a Rare Isolate with Multiple Novel Large Genomic Islands

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ABSTRACT We present here the whole-genome sequence of *Shewanella* sp. WE21, an unusual omega-3 fatty acid-producing bacterium isolated from the gastrointestinal tract of the freshwater fish *Sander vitreus* (walleye). This genome contains a number of unique, large genomic islands with genes not present in other *Shewanella* bacteria.

Shewanella spp. are Gram-negative, motile bacilli that are found in many environments but most often in aquatic environments, particularly in marine ones. They are important for the turnover of organic material, and they are capable of dissimilatory reduction of various metals and other substances. (1). Also, several *Shewanella* strains have been reported as candidates for biotechnological applications such as omega-3 fatty acid production (2) and bioremediation of heavy metals (1). In contrast to their beneficial roles, *Shewanella* strains have been identified as major agents of fish spoilage (3) and recently as fish pathogens responsible for outbreaks of disease (4). Furthermore, they are increasingly being implicated as opportunistic human pathogens (5). *Shewanella* sp. WE21, isolated from the gastrointestinal tract of the freshwater fish species *Sander vitreus* (walleye) in Lac des Mille, Ontario, Canada (48°84'N, 90°51'W) (6), represents a novel omega-3 fatty acid-producing freshwater isolate of *Shewanella*. It appears most closely related to *S. putrefaciens* strains by phylogenetic analysis (6). However, *in silico* DNA-DNA hybridization suggests that *Shewanella* sp. WE21 is more closely related to (but distinct from) *S. baltica* species (F. Dailey, unpublished results). Here, we report the whole-genome sequence of this strain.

PacBio sequencing with 100× coverage was performed as previously described (6) for *Shewanella* sp. strain WE21. Annotation was performed by using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (7). Additionally, the genomes were analyzed on the Rapid Annotations using Subsystems Technology (RAST) server (8). Acquired antibiotic resistance genes were identified by using ResFinder version 2.1 (9), virulence factors by using VirulenceFinder version 1.2 (10), clustered regularly interspaced short palindromic repeat (CRISPR) arrays by using CRISPRFinder (11), genomic islands by using IslandViewer version 4 (12), and prophage-related sequences by using PHASTER (13).

The final assembly for *Shewanella* sp. strain WE21 resulted in one large closed contig with a total length of 5,266,746 bp and a G+C content of 45.3%. Genome annotation resulted in 4,416 coding sequences (CDSs) plus one potential overlapping CDS, 105 tRNAs, 176 pseudogenes, and 31 rRNAs; 96.2% of the CDSs were classified as hypothetical proteins. Five prophage-like elements between 33.7 to 43.4 kb in length were detected. No virulence factors were identified in these prophage sequences. In addition, four genomic islands of 131.4 kb, 106.5 kb, 28.7 kb, and 9.2 kb, which have GC% contents of 40.6, 42.3, 38.3, and 57.9, respectively, were identified. In the first genomic island, we detected genes encoding putative virulence factors found in *Vibrio anguill-*

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larum (14) and other fish pathogens, as well as a type III secretion system with large overlapping genes. Analysis of the second reveals not only additional genes encoding vibrio-like virulence factors, such as *cnf2*, but also genes encoding insecticidal toxins (15) and polyketides. The third genomic island putatively encodes very novel pili, and the fourth encodes copper efflux genes. Antibiotic resistance genes penicillin (*BL*) and fluoroquinolones (*parC*, *parE*, *gyrA*, and *gyrB*) were detected. Also, cobalt-zinc-cadmium resistance genes (*CzcD*, *CzcA*, *CusA*, *CusB*, and *TR*) and arsenic resistance genes were identified. No CRISPR arrays or plasmids were detected. This genome sequence can facilitate the understanding of symbiosis and virulence in fish intestinal bacteria.

Accession number(s). The draft genome sequence of *Shewanella* sp. strain WE21 can be accessed under the GenBank accession number [CP023019](https://doi.org/10.1093/nar/gkt1226). The version described in this paper is the first version.

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